



## Figure 1A

Query = C54D2.5 CE02562 CALCIUM CHANNEL ALPHA-1 SUBUNIT LG:6  
Database: Non-redundant Database of GenBank EST Division  
824,500 sequences; 302,742,428 total letters.

H55225 CHR220164 Homo sapiens genomic clone C22\_207 5'.  
Length = 168

Plus Strand HSPs:

Score = 136 (63.8 bits), Expect =  $2.5e-10$ ,  $P = 2.5e-10$   
Identities = 23/31 (74%), Positives = 29/31 (93%), Frame = +1

Query: 440 VISLEGWTDIMYYVQDAHSFWNWIYFVLLIV 470 SEQ ID NO. 24  
VI LEGW IMYYV DAHSF N IYF LLI  
Sbjct: 1 VITLEGWVEIMYYVMDAHSFYNFYIFILLII 93 SEQ ID NO. 25

H55617 CHR220556 Homo sapiens genomic clone C22\_757 5'.  
Length = 98  
Plus Strand HSPs:

Score = 102 (47.9 bits), Expect =  $2.8e-05$ ,  $P = 2.8e-05$   
Identities = 19/23 (82%), Positives = 23/23 (100%), Frame = +2

Query: 243 NINLTAIRTVRVLRPLRAVNRIP 265 SEQ ID NO. 26  
NINL AIRTVRVLRPL A NR P  
Sbjct: 29 NINLSAIRTVRVLRPLKAINRVP 97 SEQ ID NO. 27

H55223 CHR220162 Homo sapiens genomic clone C22\_204 5'.  
Length = 94  
Plus Strand HSPs:

Score = 87 (40.8 bits), Expect = 0.0039,  $P = 0.0039$   
Identities = 14/19 (73%), Positives = 18/19 (94%), Frame = +2

Query: 154 MAVIMINCVTLGMYRPCED 172 SEQ ID NO. 28  
M VI NCVTLGMY PC D  
Sbjct: 2 MLVILLNCVTLGMYQPCDD 58 SEQ ID NO. 29



## Figure 1B

H55544 CHR220483 Homo sapiens genomic clone C22\_651 5'

Length = 123

Plus Strand HSPs:

Score = 65 (30.5 bits), Expect = 3.8, P = 0.98

Identities = 12/23 (52%), Positives = 18/23 (78%), Frame = +1

Query: 246 LTAIRTVRVLRLPLRAVNRIIPSMR 268 SEQ ID NO.30

RT R LRPLRA R MR

Sbjct: 55 IKSLRTLRLALRPLRALSRLFEGMR 123 SEQ ID NO.31

F07776| HSC2HD061 H. sapiens partial cDNA sequence; clone c-2hd06

Length = 343

Plus Strand HSPs:

Score = 100 (46.9 bits), Expect = 0.00057, P = 0.00057

Identities = 21/41 (51%), Positives = 31/41 (75%), Frame = +3

Query: 1480 PTIIRVMRVLRIARVLKLLKMAKGIRSLDDTVGEALPQVGN 1520 SEQ ID NO.32

PT+ RV+R+ RI R+L+L+K AKGIR+LL + +LP + N

Sbjct: 57 PTLXRVIRLARIGRILRLIKGAKGIRTLLFALMMSLPALFN 179 SEQ ID NO.33